

SEQUENCE LISTING

<110> Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN

5 <120> Chlamydia antigens and corresponding DNA fragments and uses thereof

<130> 77813-27

<140>

10 <141>

<150> US 60/154,652

<151> 1999-09-20

15 <160> 4

<170> PatentIn Ver. 2.0

<210> 1

20 <211> 1907

<212> DNA

<213> Chlamydia pneumoniae

<220>

25 <221> CDS

<222> (101)..(1804)

<400> 1

30 gtggcttgat tttgaaaaag gtccatggat gtgtttataa tgttcaagggt ctccctatcc 60
 aaacattgaa atacttgcta gaggagttga acatcgatct atg gga cta ttc cat 115
 Met Gly Leu Phe His
 1 5
 35 cta act ctc ttt gga ctt tta ttg tgt agt ctt ccc att tct ctt gtt 163
 Leu Thr Leu Phe Gly Leu Leu Leu Cys Ser Leu Pro Ile Ser Leu Val
 10 15 20
 40 gct aaa ttc cct gag tct gta ggt cat aag atc ctt tat ata agt acg 211
 Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile Leu Tyr Ile Ser Thr
 25 30 35
 45 caa tct aca cag cag gcc tta gca aca tat ctg gaa gct cta gat gcc 259
 Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu Glu Ala Leu Asp Ala
 40 45 50
 50 tac ggt gat cat gac ttc ttc gtt tta aga aaa atc gga gaa gac tat 307
 Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys Ile Gly Glu Asp Tyr
 55 60 65
 55 ctc aag caa agc atc cac tcc tca gat ccg caa act aga aaa agc acc 355
 Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln Thr Arg Lys Ser Thr
 70 75 80 85
 60 atc att gga gca ggc ctg gcg gga tct tca gaa gcc ttg gac gtg ctc 403
 Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu Ala Leu Asp Val Leu
 90 95 100
 60 tcc caa gct atg gaa act gca gac ccc ctg cag cag cta ctg gtt tta 451
 Ser Gln Ala Met Glu Thr Ala Asp Pro Leu Gln Gln Leu Leu Val Leu
 105 110 115

	tcg gca gtc tca gga cat ctt ggg aaa act tct gac gac tta ctg ttt	499
	Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser Asp Asp Leu Leu Phe	
	120 125 130	
5	aaa gct tta gca tct ccc tat cct gtc atc cgc tta gaa gcc gcc tat	547
	Lys Ala Leu Ala Ser Pro Tyr Pro Val Ile Arg Leu Glu Ala Ala Tyr	
	135 140 145	
10	aga ctt gct aat ttg aag aac act aaa gtc att gat cat cta cat tct	595
	Arg Leu Ala Asn Leu Lys Asn Thr Lys Val Ile Asp His Leu His Ser	
	150 155 160 165	
15	ttc att cat aag ctt ccc gaa gaa atc caa tgc cta tct gcg gca ata	643
	Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys Leu Ser Ala Ala Ile	
	170 175 180	
20	ttc cta cgc ttg gag act gaa gaa tct gat gct tat att cgg gat ctc	691
	Phe Leu Arg Leu Glu Thr Glu Glu Ser Asp Ala Tyr Ile Arg Asp Leu	
	185 190 195	
25	tta gct gcc aag aaa agc gcg att cgg agt gcc aca gct ttg cag atc	739
	Leu Ala Ala Lys Lys Ser Ala Ile Arg Ser Ala Thr Ala Leu Gln Ile	
	200 205 210	
30	gga gaa tac caa caa aaa cgc ttt ctt ccg aca ctt agg aat ttg cta	787
	Gly Glu Tyr Gln Gln Lys Arg Phe Leu Pro Thr Leu Arg Asn Leu Leu	
	215 220 225	
35	acg agt gcg tct cct caa gat caa gaa gct att ctt tat gct tta ggg	835
	Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile Leu Tyr Ala Leu Gly	
	230 235 240 245	
40	aag ctt aag gat ggt cag agc tac tac aat ata aaa aag caa ttg cag	883
	Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile Lys Lys Gln Leu Gln	
	250 255 260	
45	aag cct gat gtg gat gtc act tta gca gca gct caa gct tta att gct	931
	Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala Gln Ala Leu Ile Ala	
	265 270 275	
50	ttg ggg aaa gaa gag gac gct ctt ccc gtg ata aaa aag caa gca ctt	979
	Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile Lys Lys Gln Ala Leu	
	280 285 290	
55	gag gag cgg cct cga gcc ctg tat gcc tta cgg cat cta ccc tct gag	1027
	Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg His Leu Pro Ser Glu	
	295 300 305	
60	ata ggg att ccg att gcc ctg ccg ata ttc cta aaa act aag aac agc	1075
	Ile Gly Ile Pro Ile Ala Leu Pro Ile Phe Leu Lys Thr Lys Asn Ser	
	310 315 320 325	
65	gaa gcc aag ttg aat gta gct tta gct ctc tta gag tta ggg tgt gac	1123
	Glu Ala Lys Leu Asn Val Ala Leu Ala Leu Leu Glu Leu Gly Cys Asp	
	330 335 340	
70	acc cct aaa cta ctg gaa tac att acc gaa agg ctt gtc caa cca cat	1171
	Thr Pro Lys Leu Leu Glu Tyr Ile Thr Glu Arg Leu Val Gln Pro His	
	345 350 355	

		tat	aat	gag	act	cta	gcc	ttg	agt	ttc	tct	aag	ggg	cgt	act	tta	caa	1219
		Tyr	Asn	Glu	Thr	Leu	Ala	Leu	Ser	Phe	Ser	Lys	Gly	Arg	Thr	Leu	Gln	
				360				365						370				
5		aat	tgg	aag	cgg	gtg	aac	atc	ata	gtc	cct	caa	gat	ccc	cag	gag	agg	1267
		Asn	Trp	Lys	Arg	Val	Asn	Ile	Ile	Val	Pro	Gln	Asp	Pro	Gln	Glu	Arg	
			375					380					385					
10		gaa	agg	ttg	ctc	tcc	aca	acc	cga	ggg	ctt	gaa	gag	cag	atc	ctt	acg	1315
		Glu	Arg	Leu	Leu	Ser	Thr	Thr	Arg	Gly	Leu	Glu	Glu	Gln	Ile	Leu	Thr	
			390				395					400					405	
15		ttt	ctc	ttc	cgc	cta	cct	aaa	gaa	gct	tac	ctc	ccc	tgt	att	tat	aag	1363
		Phe	Leu	Phe	Arg	Leu	Pro	Lys	Glu	Ala	Tyr	Leu	Pro	Cys	Ile	Tyr	Lys	
					410						415					420		
20		ctt	ttg	gcg	agt	cag	aaa	act	cag	ctt	gcc	act	act	gcg	att	tct	ttt	1411
		Leu	Leu	Ala	Ser	Gln	Lys	Thr	Gln	Leu	Ala	Thr	Thr	Ala	Ile	Ser	Phe	
					425					430					435			
25		tta	agt	cac	acc	tca	cat	cag	gaa	gcc	tta	gat	cta	ctt	ttc	caa	gct	1459
		Leu	Ser	His	Thr	Ser	His	Gln	Glu	Ala	Leu	Asp	Leu	Leu	Phe	Gln	Ala	
				440				445						450				
30		gcg	aag	ctt	cct	gga	gaa	cct	atc	atc	cgc	gcc	tat	gca	gat	ctt	gct	1507
		Ala	Lys	Leu	Pro	Gly	Glu	Pro	Ile	Ile	Arg	Ala	Tyr	Ala	Asp	Leu	Ala	
			455				460						465					
35		att	tat	aat	ctc	acc	aaa	gat	cct	gaa	aaa	aaa	cgt	tct	ctc	cat	gat	1555
		Ile	Tyr	Asn	Leu	Thr	Lys	Asp	Pro	Glu	Lys	Lys	Arg	Ser	Leu	His	Asp	
			470				475					480					485	
40		tat	gca	aaa	aag	cta	att	cag	gaa	acc	ttg	tta	ttt	gtg	gac	acg	gaa	1603
		Tyr	Ala	Lys	Lys	Leu	Ile	Gln	Glu	Thr	Leu	Leu	Phe	Val	Asp	Thr	Glu	
					490						495					500		
45		aac	caa	aga	ccc	cat	ccc	agc	atg	ccc	tat	cta	cgt	tat	cag	gtc	acc	1651
		Asn	Gln	Arg	Pro	His	Pro	Ser	Met	Pro	Tyr	Leu	Arg	Tyr	Gln	Val	Thr	
				505						510					515			
50		cca	gaa	agc	cgt	acg	aag	ctc	atg	ttg	gat	att	cta	gag	aca	cta	gcc	1699
		Pro	Glu	Ser	Arg	Thr	Lys	Leu	Met	Leu	Asp	Ile	Leu	Glu	Thr	Leu	Ala	
				520				525						530				
55		acc	tcg	aag	tct	tcc	gaa	gat	atc	cgt	tta	ttg	ata	caa	ctg	atg	acg	1747
		Thr	Ser	Lys	Ser	Ser	Glu	Asp	Ile	Arg	Leu	Leu	Ile	Gln	Leu	Met	Thr	
			535				540						545					
60		gaa	gga	gat	gca	aaa	aat	ttc	cca	gtc								

<210> 2
 <211> 568
 <212> PRT
 <213> Chlamydia pneumoniae

5

<400> 2
 Met Gly Leu Phe His Leu Thr Leu Phe Gly Leu Leu Leu Cys Ser Leu
 1 5 10 15

10 Pro Ile Ser Leu Val Ala Lys Phe Pro Glu Ser Val Gly His Lys Ile
 20 25 30

Leu Tyr Ile Ser Thr Gln Ser Thr Gln Gln Ala Leu Ala Thr Tyr Leu
 35 40 45

15 Glu Ala Leu Asp Ala Tyr Gly Asp His Asp Phe Phe Val Leu Arg Lys
 50 55 60

20 Ile Gly Glu Asp Tyr Leu Lys Gln Ser Ile His Ser Ser Asp Pro Gln
 65 70 75 80

Thr Arg Lys Ser Thr Ile Ile Gly Ala Gly Leu Ala Gly Ser Ser Glu
 85 90 95

25 Ala Leu Asp Val Leu Ser Gln Ala Met Glu Thr Ala Asp Pro Leu Gln
 100 105 110

Gln Leu Leu Val Leu Ser Ala Val Ser Gly His Leu Gly Lys Thr Ser
 115 120 125

30 Asp Asp Leu Leu Phe Lys Ala Leu Ala Ser Pro Tyr Pro Val Ile Arg
 130 135 140

35 Leu Glu Ala Ala Tyr Arg Leu Ala Asn Leu Lys Asn Thr Lys Val Ile
 145 150 155 160

Asp His Leu His Ser Phe Ile His Lys Leu Pro Glu Glu Ile Gln Cys
 165 170 175

40 Leu Ser Ala Ala Ile Phe Leu Arg Leu Glu Thr Glu Glu Ser Asp Ala
 180 185 190

Tyr Ile Arg Asp Leu Leu Ala Ala Lys Lys Ser Ala Ile Arg Ser Ala
 195 200 205

45 Thr Ala Leu Gln Ile Gly Glu Tyr Gln Gln Lys Arg Phe Leu Pro Thr
 210 215 220

50 Leu Arg Asn Leu Leu Thr Ser Ala Ser Pro Gln Asp Gln Glu Ala Ile
 225 230 235 240

Leu Tyr Ala Leu Gly Lys Leu Lys Asp Gly Gln Ser Tyr Tyr Asn Ile
 245 250 255

55 Lys Lys Gln Leu Gln Lys Pro Asp Val Asp Val Thr Leu Ala Ala Ala
 260 265 270

Gln Ala Leu Ile Ala Leu Gly Lys Glu Glu Asp Ala Leu Pro Val Ile
 275 280 285

60 Lys Lys Gln Ala Leu Glu Glu Arg Pro Arg Ala Leu Tyr Ala Leu Arg
 290 295 300

44

[illegible]

<210> 4
<211> 36
<212> DNA
5 <213> Artificial Sequence
<220> primer
<223> 3' PCR primer

10 <400> 4
gcgccggatc cctccacaa ttttatgag taagcc

36

cctccacaa ttttatgag taagcc